

Figure 1: Protein alignment of Rho small GTPases from *Oryza sativa* cv. Noppon-Brarre (a japonica rice), *Brassica napus* cv. "AC Excel" "Quantum" and "Cresor" (canola), and *Glycine max* cv. Resnick (soybean). Boxes (dotted line) represent the identical amino acid.

BN41992996	(1)	-----MSARFIRGTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VVVNGATVNLGLWDTAGQEDYNRIRRL
BN42135991	(1)	-----MSARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
BN42385898	(1)	-----MSARFIRGTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VVVNGATVNLGLWDTAGQEDYNRIRRL
BN42519337	(1)	-----MSTARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
BN42557868	(1)	-----MSASVAAASVSTTTAATFIKGVTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VLVDGKTVNLGLWDTAGQEDYNRIRRL
BN43381801	(1)	-----MASTASKFIRGTVGCGAVGKTCMLICYTSNKPTDYIPTVFDNFESAN--VVVEGTTVNLGLWDTAGQEDYNRIRRL
BN44062474	(1)	-----MASSASKFIRGTVGCGAVGKTCMLICYTSNKPTDYVPTVFDNFESAN--VVVEGTTVNLGLWDTAGQEDYNRIRRL
BN44504217	(1)	-----MSARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
BN45412825	(1)	-----MSARFIRGTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VIVDGNITINLGLWDTAGQEDYNRIRRL
GM47124407	(1)	-----MSTARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VTVDGNTVNLGLWDTAGQEDYNRIRRL
GM47172047	(1)	-----MSTRFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
GM48914268	(1)	-----MSARFIRGTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
GM49741326	(1)	-----MASATARFIRGTVGCGAVGKTCMLICYTSNKPTDYIPTVFDNFESAN--VVVEGTTVNLGLWDTAGQEDYNRIRRL
GM50199916	(1)	-----MSARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
GM50693528	(1)	-----MSARFIRGTVGCGAVGKTCCLLSYTSNTPTDYVPTVFDNFESAN--VVVNGSIVNLGLWDTAGQEDYNRIRRL
GM52260563	(1)	-----MSARFIRGTVGCGAVGKTCMLISYTSNTPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
OS30848846	(1)	-----MSGARKFIRGTVGCGAVGKTCMLICYISNHPPTDYIPTVFDNFESAN--VSVDGNIVNLGLWDTAGQEDYSRIRRL
OS32558796	(1)	MGCSSVVPARSTGGNNISNDNSATDSKDLRAHLLIGSGGKSCIVLRFVRCQEDPTSKVTVGASFLSQTIALEDSTIVKFEIWDTAGQERYAAIRRL
OS33960403	(1)	-----MASSARFIRGTVGCGAVGKTCMLICYTSNKPTDYVPTVFDNFESAN--VVVDGNTVNLGLWDTAGQEDYNRIRRL
OS35505384	(1)	-----MGSKPPPPQPPSVSEHLLIGGRVGGKLSLVRYVNDVHESKQEAIVQASVLTKR-LVVEGVPITLSIWDTAGQEFHAGIIRRL
OS37807380	(1)	-----MSSAAAATRFIRGTVGCGAVGKTCMLICYTSNKPTDYIPTVFDNFESAN--VSVDSGVVNLGLWDTAGQEDYSRIRRL
YNL090W	(1)	-----MSEKAVRRKIVIIIGGAGGKTSLLYVFTLGGKFEQYHPTVFENYVTD--CRVDGIKVSITLWDTAGQEEYERIRRF

BN41992996	(74)	SRGADVFILAFSLISKASYENVSKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFVDHPCGAVPITTAQGEELMKLIGAPSYIECSSKSQENVKV	DA
BN42135991	(74)	SRGADVFILAFSLISKASYENIAKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFIDHPCGAVPITTNQGEELKKLIGSPVYIECSSKTOQNVKAV	DA
BN42395898	(74)	SRGADVFILAFSLISKASYENVSKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFVDHPCGAVPITTAQGEELMKLIGAPSYIECSSKSQENVKV	DA
BN42519337	(74)	SRGADVFILAFSLISKASYENIYKKWLPKELHYAPSIPIVLVGT	DRDD-KQFLKDHPCGAASITTAQGEELRKMIGAIKYLECSSKTOQNVKAV	DT
BN42557868	(88)	SRGADVFILAFSLISRPSPFENIAKKWPELTHYAPVPIVLVGT	DRDD-KKTFPMNYFGACTISTEQCEELRKEIGALAYIECSSKTOQNVKAV	DA
BN43381801	(76)	SRGADVFVLSFSLVSRASYENVYKKWIPELQHFAPGVPLVLVGT	DRDD-KKHYLADHPGLSPVTTAQGEELRKLIGATYIECSSKTOQNVKAV	DS
BN44062474	(76)	SRGADVFVLSFSLVSRASYENVFKKWIPELQHFAPGVPLVLVGT	DRDD-KHYLADHPGLSPVTTAQGEELRKLIGATYIECSSKTOQNVKAV	DS
BN44504217	(74)	SRGADVFILAFSLISKASYENIAKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFIDHPCGAVPITTNQGEELKKLIGSPAYIECSSKTOQNVKAV	DA
BN45412825	(74)	SRGADVFLLAFSLVSKASYENVSKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFVEHPCGAVPITTAQGEELKKVIGAPAYIECSAKTOQNVKAV	DA
GM47124407	(74)	SRGADVFLLCYSLISKASYENISKKWIPELTHYAPVPIVLVGT	DRDD-KQFLIDHPCGSARITTAQGEELKKMIGAVTYIECSSKTOQNVKAV	DA
GM47172047	(74)	SRGADVFLLAFSLISKASYENISKKWIPELTHYAPVPIVLVGT	DRDD-KQFLIDHPCGTTATATAQGEELKKAIGAAVYIECSSKTOQNVKAV	DA
GM48914268	(74)	SRGADVFILAFSLISKASYENIAKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFMDHPCGAVPITTAQGEELRKLIGAPAYIECSSKTOQNVKAV	DA
GM49741326	(77)	SRGADVFVLAFLVSLVSRASYENVLKKWIPELQHFAPGPIVLVGT	DRDD-KHYNADHPSLVPTTQGEELRKHIGATYIECSSKTOQNVKAV	DA
GM50199916	(74)	SRGADVFLLAFSLISRASASYENVAKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFQDHPCGAVPITTAQGEELRKLIGAPYIECSSKTOQNVKAV	DA
GM50693528	(74)	SRGADVFILAFSLISKASYENVSKKWIPELTHYAPGVPIVLVGT	DRDD-KQFCIDHPCGAVPITTAQGEELRKLINAPAYIECSSKTOQNVKAV	DA
GM52260563	(74)	SRGADVFLLAFSLISRASASYENVAKKWIPELTHYAPGVPIVLVGT	DRDD-KQFFQDHPCGAVPITTAQGEELRKLIGAPYIECSSKTOQNVKAV	DA
OS30848846	(75)	SRGADIFVLAFLISRASASYENVLKKWPELRRFAPVPIVLVGT	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT
OS32558796	(101)	YRGAAAADVVDITSPESFSKAQYWKELQKHGSPDIIMVLVGT	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT
OS33960403	(76)	SRGADVFVLAFLVSLVSRASYENVMKKWIPELQHYAPGVPIVLVGT	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT
OS35505384	(83)	YRGDAALLVVDITDNTFLRTVKWKELQKQANKOIVMALAANIS	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT
OS37807380	(78)	SRGADVFILSFLISRASASYENVQKKWPELRRFAPGVPIVLVGT	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT
YNL090W	(75)	YSKADITILIGFAVDNFESLINARTKWADEALRYCPDAPIVLVGT	DRDH-RSYLADHPAASATTAQGEELRKOIGAAAYIECSSKTOQNVKAV	DT

BN41992996 (173) AIRVVLQPPKQK---KKGK---QKACSIL-----
BN42135991 (173) AIKVVLPKPSKK-----KKKN---KNRCVFL-----
BN42385898 (173) AIRVVLQPPKQK---KSKA---QKACSIL-----
BN42519337 (173) AIRVALRPPKAKK---IKPLRTKRSRTCTFF-----
BN42557868 (187) AIKVVLPPTKIK---KQRR---FRECHAL-----
BN43381801 (176) AIKEVIKPVVKQKEKTQTKKQKS-NHGCLSNVLCGRIVTRH-----
BN44062474 (175) AIKEVIKPVVKQKGTKKKQKQSNHHGCLSNVLCGRIVTRH-----
BN44504217 (173) AIKVVLPKQK---KKK---KNGCVFL-----
BN45412825 (173) AIKVVLPKPKKKR---KKRKS---QKACSIL-----
GM47112407 (173) AIKVALKPPKPKK---PR---KKRTCTFL-----
GM47112047 (173) AIKVVLPKPSKK---GK---KNTPCVFL-----
GM48914268 (173) AIKVVLPKPKK---KRKT---QKACSIL-----
GM49741326 (176) AIRMVIKPPKQKQNE---KRKKPR---GCFLNVLCRRNIVRLK---
GM50199916 (173) AIKVVLPKQK---KKRG---QKACSIL-----
GM50693528 (173) AIRVVLQPPKQK---KKGK---QKACSIL-----
GM52260563 (173) AIKVVLPKQK---KKRG---QKACSIL-----
OS30848846 (174) AIKVVLPKRRRGETTMARKTTRRSTGCSLKNLMCGSACV-----
OS32558796 (189) IAKRLPRTAS-----
OS33960403 (175) AIKVIKPTKORDR---KKKTTRGCSFFCKGVMRRRLVCFK---
OS35505384 (171) IAKRLLERRKNSS---DGLSLAHPKKGLIIVDDEPEKEPPKCCS
OS37807380 (177) AIKVVLPKPR---HKDVTTRKKLQSSSNRPVRYFCGSACFA-----
YNL090W (173) ATFTSLMKKEPG-----ANCCIL-----